

# SEQUENCE LISTING

<110> Kaia Palm  
Tonis Timmusk  
CeMines Research

<120> MAMMALIAN NEURALIZED FAMILY OF  
TRANSCRIPTION REGULATORS AND USES THEREFOR

<130> CEMRES.001A

<160> 48

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1725

<212> DNA

<213> Homo sapien

<400> 1

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<211> 574

<212> PRT  
<213> Homo sapien

<400> 2

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          35          40          45
Cys Pro Ala Val Leu Pro Ser Gly Gly Leu Pro Ala Thr Pro Leu Leu
          50          55          60
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His
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Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser
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Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly
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Leu Thr Arg Gly Val Gln Leu Leu Asp Ser Glu Leu Val Leu Pro Asp
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Cys Leu Arg Pro Arg Ser Phe Thr Ala Leu Arg Arg Pro Ser Leu Arg
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Arg Glu Ala Asp Asp Ala Arg Leu Ser Val Ser Leu Cys Asp Leu Asn
          245          250          255
Val Pro Gly Ala Asp Gly Asp Glu Ala Ala Pro Ala Ala Gly Cys Pro
          260          265          270
Ile Pro Gln Asn Ser Leu Asn Ser Gln His Ser Arg Ala Leu Pro Ala
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Gln Leu Asp Gly Asp Leu Arg Phe His Ala Leu Arg Ala Gly Ala His
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Asp Glu Arg Ala Leu Val Phe Thr Ser Arg Pro Val Arg Val Ala Glu
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Thr Ile Phe Val Lys Val Thr Arg Ser Gly Gly Ala Arg Pro Gly Ala
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Leu Ser Phe Gly Val Thr Thr Cys Asp Pro Gly Thr Leu Arg Pro Ala
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Asp Leu Pro Phe Ser Pro Glu Ala Leu Val Asp Arg Lys Glu Phe Trp
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 Thr Ala Pro Asn Ser Pro Val Ser Leu Pro Glu Ser Pro Val Thr Pro  
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 Gly Leu Gly Gln Trp Ser Asp Glu Cys Thr Ile Cys Tyr Glu His Ala  
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 <211> 1674  
 <212> DNA  
 <213> Homo sapien

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 <212> PRT  
 <213> Homo sapien

<400> 4  
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 35 40 45  
 His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His Lys  
 50 55 60  
 Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser Asn  
 65 70 75 80  
 Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys Lys  
 85 90 95  
 Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys Asp  
 100 105 110  
 Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro Asp  
 115 120 125  
 Leu Val Ser Gln Ser Gly Phe Trp Ala Lys Ala Leu Pro Glu Glu Phe  
 130 135 140  
 Ala Asn Glu Gly Asn Ile Ala Phe Trp Val Asp Lys Lys Gly Arg  
 145 150 155 160  
 Val Phe His Arg Ile Asn Asp Ser Ala Val Met Leu Phe Phe Ser Gly  
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 Val Arg Thr Ala Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly Leu  
 180 185 190  
 Thr Arg Gly Val Gln Leu Leu Asp Ser Glu Leu Val Leu Pro Asp Cys  
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 Glu Ala Asp Asp Ala Arg Leu Ser Val Ser Leu Cys Asp Leu Asn Val  
 225 230 235 240  
 Pro Gly Ala Asp Gly Asp Glu Ala Ala Pro Ala Ala Gly Cys Pro Ile  
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 Pro Gln Asn Ser Leu Asn Ser Gln His Ser Arg Ala Leu Pro Ala Gln  
 260 265 270  
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 275 280 285  
 Arg Ile Leu Asp Glu Gln Thr Val Ala Arg Val Glu His Gly Arg Asp  
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 Glu Arg Ala Leu Val Phe Thr Ser Arg Pro Val Arg Val Ala Glu Thr  
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 Ile Phe Val Lys Val Thr Arg Ser Gly Gly Ala Arg Pro Gly Ala Leu  
 325 330 335  
 Ser Phe Gly Val Thr Thr Cys Asp Pro Gly Thr Leu Arg Pro Ala Asp  
 340 345 350  
 Leu Pro Phe Ser Pro Glu Ala Leu Val Asp Arg Lys Glu Phe Trp Ala  
 355 360 365

1620  
 1674

Val Cys Arg Val Pro Gly Pro Leu His Ser Gly Asp Ile Leu Gly Leu  
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 Val Val Asn Ala Asp Gly Glu Leu His Leu Ser His Asn Gly Ala Ala  
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 Ala Gly Met Gln Leu Cys Val Asp Ala Ser Gln Pro Leu Trp Met Leu  
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 Phe Gly Leu His Gly Thr Ile Thr Gln Ile Arg Ile Leu Gly Ser Thr  
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 Ile Leu Ala Glu Arg Gly Ile Pro Ser Leu Pro Cys Ser Pro Ala Ser  
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 Thr Pro Thr Ser Pro Ser Ala Leu Gly Ser Arg Leu Ser Asp Pro Leu  
 450 455 460  
 Leu Ser Thr Cys Ser Ser Gly Pro Leu Gly Ser Ser Ala Gly Gly Thr  
 465 470 475 480  
 Ala Pro Asn Ser Pro Val Ser Leu Pro Glu Ser Pro Val Thr Pro Gly  
 485 490 495  
 Leu Gly Gln Trp Ser Asp Glu Cys Thr Ile Cys Tyr Glu His Ala Val  
 500 505 510  
 Asp Thr Val Ile Tyr Thr Cys Gly His Met Cys Leu Cys Tyr Ala Cys  
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 <213> Homo sapien

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<212> PRT  
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<400> 6

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          35          40          45
Pro Ser Leu Arg Arg Glu Ala Asp Asp Ala Arg Leu Ser Val Ser Leu
          50          55          60
Cys Asp Leu Asn Val Pro Gly Ala Asp Gly Asp Glu Ala Ala Pro Ala
65          70          75          80
Ala Gly Cys Pro Ile Pro Gln Asn Ser Leu Asn Ser Gln His Ser Arg
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Ala Leu Pro Ala Gln Leu Asp Gly Asp Leu Arg Phe His Ala Leu Arg
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Ala Gly Ala His Val Arg Ile Leu Asp Glu Gln Thr Val Ala Arg Val
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Glu His Gly Arg Asp Glu Arg Ala Leu Val Phe Thr Ser Arg Pro Val
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145          150          155          160
Arg Pro Gly Ala Leu Ser Phe Gly Val Thr Thr Cys Asp Pro Gly Thr
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Leu Arg Pro Ala Asp Leu Pro Phe Ser Pro Glu Ala Leu Val Asp Arg
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Lys Glu Phe Trp Ala Val Cys Arg Val Pro Gly Pro Leu His Ser Gly
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Asp Ile Leu Gly Leu Val Val Asn Ala Asp Gly Glu Leu His Leu Ser
210          215          220
His Asn Gly Ala Ala Ala Gly Met Gln Leu Cys Val Asp Ala Ser Gln
225          230          235          240
Pro Leu Trp Met Leu Phe Gly Leu His Gly Thr Ile Thr Gln Ile Arg
          245          250          255
Ile Leu Gly Ser Thr Ile Leu Ala Glu Arg Gly Ile Pro Ser Leu Pro
          260          265          270
Cys Ser Pro Ala Ser Thr Pro Thr Ser Pro Ser Ala Leu Gly Ser Arg
          275          280          285
Leu Ser Asp Pro Leu Leu Ser Thr Cys Ser Ser Gly Pro Leu Gly Ser
          290          295          300
Ser Ala Gly Gly Thr Ala Pro Asn Ser Pro Val Ser Leu Pro Glu Ser
305          310          315          320
Pro Val Thr Pro Gly Leu Gly Gln Trp Ser Asp Glu Cys Thr Ile Cys
          325          330          335
Tyr Glu His Ala Val Asp Thr Val Ile Tyr Thr Cys Gly His Met Cys
          340          345          350
Leu Cys Tyr Ala Cys Gly Leu Arg Leu Lys Lys Ala Leu His Ala Cys
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 <211> 1749  
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 <213> mouse

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 50 55 60  
 Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His  
 65 70 75 80  
 Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser





Val Asp Thr Val Ile Tyr Thr Cys Gly His Met Cys Leu Cys Tyr Ser  
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 <212> DNA  
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 <213> mouse

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Arg	Pro	Val	Leu	Ile	Tyr	Glu	Gln	Val	Arg	Leu	Lys	Ile	Thr	Lys	Lys
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Pro	Gln	Asn	Ser	Leu	Asn	Ser	Gln	His	Ser	Arg	Ala	Leu	Pro	Ala	Gln
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Ser	Phe	Gly	Val	Thr	Thr	Cys	Asp	Pro	Gly	Thr	Leu	Arg	Pro	Ala	Asp
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Leu	Pro	Phe	Ser	Pro	Glu	Ala	Leu	Val	Asp	Arg	Lys	Glu	Phe	Trp	Ala
		355					360					365			
Val	Cys	Arg	Val	Pro	Gly	Pro	Leu	His	Ser	Gly	Asp	Ile	Leu	Gly	Leu
	370					375					380				
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Leu Gly Gln Trp Ser Asp Glu Cys Thr Ile Cys Tyr Glu His Ala Val  
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Asp Thr Val Ile Tyr Thr Cys Gly His Met Cys Leu Cys Tyr Ser Cys  
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<212> DNA  
<213> mouse

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ctcatctacg agcaagtcag gctgaagatc accaagaagc aatgctgctg gagcggggcc 360  
ctgcgacttg gcttcaccag caaggaccct tcccgcattc accccgactc gctgcccag 420  
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<211> 344  
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<213> mouse

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Cys Pro Pro Thr Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu  
50 55 60  
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His  
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Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser  
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Asn Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys  
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 Lys Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys  
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 Asp Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro  
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 145 150 155 160  
 Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly  
 165 170 175  
 Arg Val Phe Tyr Arg Ile Asn Glu Ser Ala Ala Met Leu Phe Phe Ser  
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 Gly Val Arg Thr Val Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly  
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 260 265 270  
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 Thr Cys Gly His Met Cys Leu Cys Tyr Ser Cys Gly Leu Arg Leu Lys  
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<210> 13

<211> 876

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<400> 13

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<400> 14

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Gly	Ser	Phe	Pro	Val	Pro	Ser	His	Arg	Cys	His	His	Lys	Gln	Lys	His
		35					40					45			
Cys	Pro	Pro	Thr	Leu	Ser	Gly	Gly	Gly	Leu	Pro	Ala	Thr	Pro	Leu	Leu
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Phe	His	Pro	His	Thr	Lys	Gly	Ser	Gln	Ile	Leu	Met	Asp	Leu	Ser	His
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Lys	Ala	Val	Lys	Arg	Gln	Ala	Ser	Phe	Cys	Asn	Ala	Ile	Thr	Phe	Ser
				85					90					95	
Asn	Arg	Pro	Val	Leu	Ile	Tyr	Glu	Gln	Val	Arg	Leu	Lys	Ile	Thr	Lys
			100					105					110		
Lys	Gln	Cys	Cys	Trp	Ser	Gly	Ala	Leu	Arg	Leu	Gly	Phe	Thr	Ser	Lys
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Asp	Pro	Ser	Arg	Ile	His	Pro	Asp	Ser	Leu	Pro	Lys	Tyr	Ala	Cys	Pro
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Phe	Ala	Asn	Glu	Gly	Asn	Ile	Ile	Ala	Phe	Trp	Val	Asp	Lys	Lys	Gly
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Arg	Val	Phe	Tyr	Arg	Ile	Asn	Glu	Ser	Ala	Ala	Met	Leu	Phe	Phe	Ser
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Gly	Val	Arg	Thr	Val	Asp	Pro	Leu	Trp	Ala	Leu	Val	Asp	Val	Tyr	Gly
		195					200					205			
Leu	Thr	Arg	Gly	Val	Gln	Leu	Leu	Asp	Ser	Glu	Leu	Val	Leu	Pro	Glu
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225					230					235					240
Cys	Tyr	Glu	His	Ala	Val	Asp	Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met
				245					250					255	
Cys	Leu	Cys	Tyr	Ser	Cys	Gly	Leu	Arg	Leu	Lys	Lys	Ala	Leu	His	Ala
			260				265						270		
Cys	Cys	Pro	Ile	Cys	Arg	Arg	Pro	Ile	Lys	Asp	Ile	Ile	Lys	Thr	Tyr
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 <212> DNA  
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<400> 15

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<211> 574

<212> PRT

<213> rat

<400> 16

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Ser	Ser	Phe	Pro	Val	Pro	Ser	His	Arg	Cys	His	His	Lys	Gln	Lys	His
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Cys	Pro	Pro	Ala	Leu	Ser	Gly	Gly	Gly	Leu	Pro	Ala	Thr	Pro	Leu	Leu
	50					55					60				
Phe	His	Pro	His	Thr	Lys	Gly	Ser	Gln	Ile	Leu	Met	Asp	Leu	Ser	His
65				70					75					80	
Lys	Ala	Val	Lys	Arg	Gln	Ala	Ser	Phe	Cys	Asn	Ala	Ile	Thr	Phe	Ser
			85					90					95		
Asn	Arg	Pro	Val	Leu	Ile	Tyr	Glu	Gln	Val	Arg	Leu	Lys	Ile	Thr	Lys
		100					105					110			
Lys	Gln	Cys	Cys	Trp	Ser	Gly	Ala	Leu	Arg	Leu	Gly	Phe	Thr	Ser	Lys
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Asp	Pro	Ser	Arg	Ile	His	Pro	Asp	Ser	Leu	Pro	Lys	Tyr	Ala	Cys	Pro
	130				135					140					
Asp	Leu	Val	Ser	Gln	Ser	Gly	Phe	Trp	Ala	Lys	Ala	Leu	Pro	Glu	Glu
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Gly	Val	Arg	Thr	Ala	Asp	Pro	Leu	Trp	Ala	Leu	Val	Asp	Val	Tyr	Gly		
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Cys	Glu	Ala	Asp	Glu	Ala	Arg	Leu	Ser	Val	Ser	Leu	Cys	Asp	Leu	Asn		
			245						250					255			
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	275					280						285					
Gln	Leu	Asp	Gly	Asp	Leu	Arg	Phe	His	Ala	Leu	Arg	Ala	Arg	Ala	Gln		
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Val	Arg	Ile	Leu	Asp	Glu	Gln	Thr	Val	Ala	Arg	Leu	Glu	His	Gly	Arg		
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			325						330					335			
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Leu	Ser	Phe	Gly	Val	Thr	Thr	Cys	Asp	Pro	Gly	Thr	Leu	Arg	Pro	Ala		
	355						360					365					
Asp	Leu	Pro	Phe	Ser	Pro	Glu	Ala	Leu	Val	Asp	Arg	Lys	Glu	Phe	Trp		
370						375					380						
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Pro	Ala	Gly	Met	Gln	Leu	Cys	Val	Asp	Ala	Ser	Gln	Pro	Leu	Trp	Met		
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<212> DNA

<213> rat

<400> 17

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acagtcattc acacgtgtgg ccacatgtgc ctgtgtact cctgtggcct gcgcctcaag 960
aaggccctgc acgcctgtcg ccccatctgc cgctcgccca tcaaggacat catcaagacc 1020
taccgcagct cctag 1035
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<210> 18

<211> 344

<212> PRT

<213> rat

<400> 18

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Met Gly Asn Asn Phe Ser Ser Val Ser Ser Leu Gln Arg Gly Asn Pro
1 5 10 15
Ser Arg Ala Ser Arg Gly His Pro Gln Asn Leu Lys Asp Ser Ile Gly
20 25 30
Ser Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His
35 40 45
Cys Pro Pro Ala Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu
50 55 60
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His
65 70 75 80
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser
85 90 95
Asn Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys
100 105 110
Lys Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys
115 120 125
Asp Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro
130 135 140
Asp Leu Val Ser Gln Ser Gly Phe Trp Ala Lys Ala Leu Pro Glu Glu
145 150 155 160
Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly
165 170 175
Arg Val Phe Tyr Arg Ile Asn Glu Ser Ala Ala Met Leu Phe Phe Ser
180 185 190
Gly Val Arg Thr Ala Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly
195 200 205
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Leu Thr Arg Gly Val Gln Leu Leu Gly Ser Thr Ile Met Ala Glu Arg  
 210 215 220  
 Gly Gly Pro Ser Leu Pro Cys Ser Pro Ala Ser Thr Pro Thr Ser Pro  
 225 230 235 240  
 Ser Ala Leu Gly Ser Arg Leu Ser Asp Pro Leu Leu Ser Thr Cys Gly  
 245 250 255  
 Ser Gly Pro Leu Gly Gly Ser Val Gly Gly Thr Ala Pro Asn Ser Pro  
 260 265 270  
 Val Ser Leu Pro Glu Ser Pro Val Thr Pro Gly Leu Gly Gln Trp Ser  
 275 280 285  
 Asp Glu Cys Thr Ile Cys Tyr Glu His Ala Val Asp Thr Val Ile Tyr  
 290 295 300  
 Thr Cys Gly His Met Cys Leu Cys Tyr Ser Cys Gly Leu Arg Leu Lys  
 305 310 315 320  
 Lys Ala Leu His Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp  
 325 330 335  
 Ile Ile Lys Thr Tyr Arg Ser Ser  
 340

<210> 19  
 <211> 888  
 <212> DNA  
 <213> rat

<400> 19  
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 cgatgccatc acaagcagaa gcattgcccg cccgcgctgt cagggtgggg gctcccggcc 180  
 acaccgctgc tcttccaccc ccacactaag ggctcccaga tcctcatgga cctcagccac 240  
 aaggccgtca agaggcaggc cagcttctgt aatgccatca ccttcagcaa ccgccccgtc 300  
 ctcatctacg agcaagtcag gctgaagatc accaagaagc agtgctgctg gagcggggcc 360  
 ctgcgacttg gcttcaccag caaggacct tcccgcattc accccgactc actgcccaag 420  
 tacgcctgcc ctgacctggg gtcccagagt ggcttctggg ccaaagcggt gcctgaggag 480  
 tttgccaacg agggcaacat cattgccttc tgggtggaca agaagggccg agtcttctac 540  
 cggatcaatg agtcggctgc catgctgttc ttcagcgggg ttcgaacggc ggaccgctc 600  
 tgggccttgg tggacgtcta tggcctcaca cgggggtgtc agctgctagg aacagcccc 660  
 aactcacctg tgagcctgcc cgagtcacca gtgaccccg gtctgggcca gtggagcgat 720  
 gaatgcacca tttgctatga acacgcagt gatacagtca tctacagtg tggccacatg 780  
 tgccctgtgt actcctgtgg cctgcgcctc aagaaggccc tgcacgcctg ctgccccatc 840  
 tgccgtcgcc ccatcaagga catcatcaag acctaccgca gtccttag 888

<210> 20  
 <211> 295  
 <212> PRT  
 <213> rat

<400> 20  
 Met Gly Asn Asn Phe Ser Ser Val Ser Ser Leu Gln Arg Gly Asn Pro  
 1 5 10 15  
 Ser Arg Ala Ser Arg Gly His Pro Gln Asn Leu Lys Asp Ser Ile Gly  
 20 25 30  
 Ser Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His  
 35 40 45  
 Cys Pro Pro Ala Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu

50		55		60	
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His					
65		70		75	80
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser					
	85		90		95
Asn Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys					
	100		105		110
Lys Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys					
	115		120		125
Asp Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro					
	130		135		140
Asp Leu Val Ser Gln Ser Gly Phe Trp Ala Lys Ala Leu Pro Glu Glu					
145		150		155	160
Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly					
	165		170		175
Arg Val Phe Tyr Arg Ile Asn Glu Ser Ala Ala Met Leu Phe Phe Ser					
	180		185		190
Gly Val Arg Thr Ala Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly					
	195		200		205
Leu Thr Arg Gly Val Gln Leu Leu Gly Thr Ala Pro Asn Ser Pro Val					
	210		215		220
Ser Leu Pro Glu Ser Pro Val Thr Pro Gly Leu Gly Gln Trp Ser Asp					
225		230		235	240
Glu Cys Thr Ile Cys Tyr Glu His Ala Val Asp Thr Val Ile Tyr Thr					
	245		250		255
Cys Gly His Met Cys Leu Cys Tyr Ser Cys Gly Leu Arg Leu Lys Lys					
	260		265		270
Ala Leu His Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Ile					
	275		280		285
Ile Lys Thr Tyr Arg Ser Ser					
	290		295		

<210> 21  
 <211> 1675  
 <212> DNA  
 <213> Homo sapien

<400> 21  
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 ttccacgcgc aggcctaaag caagaacgtg cggctggacg gccactcgcg ccgggccaca 180  
 cggcgcaaca gcttctgcaa tggcgtcacg ttcacgcagc ggccatccg gctgtacgag 240  
 caggtgcggc tgcgcctggt ggccgtgcgc cctggctgga gcggcgcgct gcgcttcggc 300  
 ttcaccgcgc acgatccgtc gctcatgagc gcccaggaca tcccaagta cgctgcccgc 360  
 gacctggtca cgcggccggg ctactgggcc aaggcactgc ccgagaacct ggcgctgcgc 420  
 gacacggtgc tggcctactg ggccgaccgc cacggccgcg tgttctacag cgtgaacgac 480  
 ggcgagccgg tgctcttcca ctgcggcggt gccgtgggcg gcccgctctg ggcgctcatt 540  
 gatgtctacg gcatcaccga cgaggtgcag cttctggaga gcgccttcgc tgacacgctg 600  
 acgcccgcgc gcctcagcca ggcccgcttc agcgctgcc tgcgcccag cagccacgac 660  
 gcggccaact tcgacaacaa cgagctcgag aacaaccagg tgggtggcaa gctggggccac 720  
 ctggcgctgg gccgcgcccc gggccaccgc ccagccgacg ccgcggccgc cgccattccg 780  
 tgccggcccc gtgacgcccc gcggccccgc tcgtcgccgg cgctactgga ggccgacctg 840  
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 gcaccgcggc ccgacggcgg ccgcacgctg gtcttctccg agcgcccgct gcggccccgc 960

gagagcctct tcgtggaggt gggcgcgtccg gggctggcgg cgcccggcgc gctggccttc 1020  
ggcatcacgt cgtgcgaccc gggcgtgcta cggcccaacg agctgcccgc cgaccagac 1080  
gcgctgctcg accgcaaaga gtactgggtg gtggcgcgcg ccggggcccg gccgagcggc 1140  
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cgtccgcgcg gccgcctgct gtgcgtcgac accacgcagg cgctctgggc cttcttcgcc 1260  
gtgcgcggcg gcgtcgcggg ccagctgcgt ctccctcggtta ccctgcagtc cagccctgcg 1320  
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ttcagtgtca accagtcctc ctcggcattc gagtcattcc tggtgacggc ccccagctcc 1440  
ccgctgagcc ccccggtgtc ccccggtgtc tccccaccgg agccggcagg catcaagaat 1500  
ggcgagtgca cgggtgtgctt cgatggcgag gtggacacgg tcatctacac gtgtggacac 1560  
atgtgcctgt gccacagctg cggcctgcgg ctcaagcgac agggccgggc ctgctgcccc 1620  
atctgccggc ggcccatcaa ggacgtcatt aagatctaca ggccatagcc tagcc 1675

<210> 22

<211> 555

<212> PRT

<213> Homo sapien

<400> 22

Met	Gly	Asn	Thr	Val	His	Arg	Thr	Leu	Pro	Asp	Pro	Ser	Pro	Pro	Ala
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Arg	Leu	Leu	Ala	Thr	Arg	Pro	Cys	Cys	Gly	Pro	Gly	Pro	Glu	Arg	Arg
			20					25					30		
Pro	Val	Leu	Gly	Glu	Ala	Pro	Arg	Phe	His	Ala	Gln	Ala	Lys	Gly	Lys
		35					40					45			
Asn	Val	Arg	Leu	Asp	Gly	His	Ser	Arg	Arg	Ala	Thr	Arg	Arg	Asn	Ser
	50					55					60				
Phe	Cys	Asn	Gly	Val	Thr	Phe	Thr	Gln	Arg	Pro	Ile	Arg	Leu	Tyr	Glu
65				70					75					80	
Gln	Val	Arg	Leu	Arg	Leu	Val	Ala	Val	Arg	Pro	Gly	Trp	Ser	Gly	Ala
			85					90						95	
Leu	Arg	Phe	Gly	Phe	Thr	Ala	His	Asp	Pro	Ser	Leu	Met	Ser	Ala	Gln
		100						105					110		
Asp	Ile	Pro	Lys	Tyr	Ala	Cys	Pro	Asp	Leu	Val	Thr	Arg	Pro	Gly	Tyr
	115					120						125			
Trp	Ala	Lys	Ala	Leu	Pro	Glu	Asn	Leu	Ala	Leu	Arg	Asp	Thr	Val	Leu
	130					135					140				
Ala	Tyr	Trp	Ala	Asp	Arg	His	Gly	Arg	Val	Phe	Tyr	Ser	Val	Asn	Asp
145				150					155						160
Gly	Glu	Pro	Val	Leu	Phe	His	Cys	Gly	Val	Ala	Val	Gly	Gly	Pro	Leu
			165					170						175	
Trp	Ala	Leu	Ile	Asp	Val	Tyr	Gly	Ile	Thr	Asp	Glu	Val	Gln	Leu	Leu
		180						185					190		
Glu	Ser	Ala	Phe	Ala	Asp	Thr	Leu	Thr	Pro	Ala	Arg	Leu	Ser	Gln	Ala
	195					200						205			
Arg	Phe	Ser	Ala	Cys	Leu	Pro	Pro	Ser	Ser	His	Asp	Ala	Ala	Asn	Phe
	210					215					220				
Asp	Asn	Asn	Glu	Leu	Glu	Asn	Asn	Gln	Val	Val	Ala	Lys	Leu	Gly	His
225				230					235						240
Leu	Ala	Leu	Gly	Arg	Ala	Pro	Gly	Pro	Pro	Pro	Ala	Asp	Ala	Ala	Ala
			245					250						255	
Ala	Ala	Ile	Pro	Cys	Gly	Pro	Arg	Glu	Arg	Pro	Arg	Pro	Ala	Ser	Ser
		260						265					270		
Pro	Ala	Leu	Leu	Glu	Ala	Asp	Leu	Arg	Phe	His	Ala	Thr	Arg	Gly	Pro
	275						280						285		

Asp Val Ser Leu Ser Ala Asp Arg Lys Val Ala Cys Ala Pro Arg Pro  
 290 295 300  
 Asp Gly Gly Arg Thr Leu Val Phe Ser Glu Arg Pro Leu Arg Pro Gly  
 305 310 315 320  
 Glu Ser Leu Phe Val Glu Val Gly Arg Pro Gly Leu Ala Ala Pro Gly  
 325 330 335  
 Ala Leu Ala Phe Gly Ile Thr Ser Cys Asp Pro Gly Val Leu Arg Pro  
 340 345 350  
 Asn Glu Leu Pro Ala Asp Pro Asp Ala Leu Leu Asp Arg Lys Glu Tyr  
 355 360 365  
 Trp Val Val Ala Arg Ala Gly Pro Val Pro Ser Gly Gly Asp Ala Leu  
 370 375 380  
 Ser Phe Thr Leu Arg Pro Gly Gly Asp Val Leu Leu Gly Ile Asn Gly  
 385 390 395 400  
 Arg Pro Arg Gly Arg Leu Leu Cys Val Asp Thr Thr Gln Ala Leu Trp  
 405 410 415  
 Ala Phe Phe Ala Val Arg Gly Gly Val Ala Gly Gln Leu Arg Leu Leu  
 420 425 430  
 Gly Thr Leu Gln Ser Ser Pro Ala Thr Thr Thr Pro Ser Gly Ser Leu  
 435 440 445  
 Ser Gly Ser Gln Asp Asp Ser Asp Ser Asp Met Thr Phe Ser Val Asn  
 450 455 460  
 Gln Ser Ser Ser Ala Ser Glu Ser Ser Leu Val Thr Ala Pro Ser Ser  
 465 470 475 480  
 Pro Leu Ser Pro Pro Val Ser Pro Val Phe Ser Pro Pro Glu Pro Ala  
 485 490 495  
 Gly Ile Lys Asn Gly Glu Cys Thr Val Cys Phe Asp Gly Glu Val Asp  
 500 505 510  
 Thr Val Ile Tyr Thr Cys Gly His Met Cys Leu Cys His Ser Cys Gly  
 515 520 525  
 Leu Arg Leu Lys Arg Gln Ala Arg Ala Cys Cys Pro Ile Cys Arg Arg  
 530 535 540  
 Pro Ile Lys Asp Val Ile Lys Ile Tyr Arg Pro  
 545 550 555

<210> 23  
 <211> 1129  
 <212> DNA  
 <213> Homo sapien

<400> 23  
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 gcgcgcctca gccaggcccc cttcagcgcc tgcctgcccgc ccagcagcca cgacgcggcc 120  
 aacttcgaca acaacgagct cgagaacaac caggtggtgg ccaagctggg ccacctggcg 180  
 ctgggcccgcg ccccgggccc accgccagcc gacgccgcgg ccgccgccat tccgtgcggg 240  
 ccccgtagac gcccgcggcc cgcgtcgtcg ccggcgctac tggaggccga cctgcgcttc 300  
 cacgcaacac gcgggcccga cgtgagcctg tcggccgacc gcaaagtggc ctgcgaccg 360  
 cgccccgacg gcggccgcac gctggtcttc tccgagcgcc cgctgcggcc cggcgagagc 420  
 ctcttcgtgg aggtgggccc tccggggctg gcggcgcccc gcgcgctggc cttcggcatc 480  
 acgtcgtgcg acccgggcgt gctacggccc aacgagctgc ccgccgaccc agacgcgctg 540  
 ctcgaccgca aagagtactg ggtggtggcg cgcgcggggc ccgtgccgag cggcggcgac 600  
 gcgctcagct tcacgctgcg gcccggcggc gacgtgctcc tgggcatcaa cgggcgtccg 660  
 cgcggccgccc tgctgtgctg cgacaccacg caggcgctct gggccttctt cgccgtgcgc 720  
 ggcggcgctg cgggcccagct gcgtctcttc ggtaccctgc agtccagccc tgcgaccacg 780

actccatcag ggtccctcag cggctcccag gacgatagtg attcagatat gaccttcagt 840  
gtcaaccagt cctcctcggc atctgagtc tccctgggtga cggccccccag ctccccgctg 900  
agccccccgg tgtcccccggt gttctcccca cggagccgg caggcatcaa gaatggcgag 960  
tgcacgggtg gcttcgatgg cgaggtggac acggtcatct acacgtgtgg acacatgtgc 1020  
ctgtgccaca gctgcggcct gcggtcaag cgacaggccc gggcctgctg ccccatctgc 1080  
cggcggccca tcaaggacgt cattaagatc tacaggccat agcctagcc 1129

<210> 24

<211> 373

<212> PRT

<213> Homo sapien

<400> 24

Met	Gly	Asn	Thr	Val	His	Arg	Thr	Leu	Pro	Glu	Ser	Ala	Phe	Ala	Asp
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Thr	Leu	Thr	Pro	Ala	Arg	Leu	Ser	Gln	Ala	Arg	Phe	Ser	Ala	Cys	Leu
			20					25					30		
Pro	Pro	Ser	Ser	His	Asp	Ala	Ala	Asn	Phe	Asp	Asn	Asn	Glu	Leu	Glu
		35					40					45			
Asn	Asn	Gln	Val	Val	Ala	Lys	Leu	Gly	His	Leu	Ala	Leu	Gly	Arg	Ala
	50					55				60					
Pro	Gly	Pro	Pro	Pro	Ala	Asp	Ala	Ala	Ala	Ala	Ile	Pro	Cys	Gly	
65					70				75					80	
Pro	Arg	Glu	Arg	Pro	Arg	Pro	Ala	Ser	Ser	Pro	Ala	Leu	Leu	Glu	Ala
				85				90						95	
Asp	Leu	Arg	Phe	His	Ala	Thr	Arg	Gly	Pro	Asp	Val	Ser	Leu	Ser	Ala
			100					105					110		
Asp	Arg	Lys	Val	Ala	Cys	Ala	Pro	Arg	Pro	Asp	Gly	Gly	Arg	Thr	Leu
		115					120					125			
Val	Phe	Ser	Glu	Arg	Pro	Leu	Arg	Pro	Gly	Glu	Ser	Leu	Phe	Val	Glu
	130					135				140					
Val	Gly	Arg	Pro	Gly	Leu	Ala	Ala	Pro	Gly	Ala	Leu	Ala	Phe	Gly	Ile
145					150					155					160
Thr	Ser	Cys	Asp	Pro	Gly	Val	Leu	Arg	Pro	Asn	Glu	Leu	Pro	Ala	Asp
				165				170						175	
Pro	Asp	Ala	Leu	Leu	Asp	Arg	Lys	Glu	Tyr	Trp	Val	Val	Ala	Arg	Ala
		180						185					190		
Gly	Pro	Val	Pro	Ser	Gly	Gly	Asp	Ala	Leu	Ser	Phe	Thr	Leu	Arg	Pro
		195					200					205			
Gly	Gly	Asp	Val	Leu	Leu	Gly	Ile	Asn	Gly	Arg	Pro	Arg	Gly	Arg	Leu
	210					215					220				
Leu	Cys	Val	Asp	Thr	Thr	Gln	Ala	Leu	Trp	Ala	Phe	Phe	Ala	Val	Arg
225					230					235					240
Gly	Gly	Val	Ala	Gly	Gln	Leu	Arg	Leu	Leu	Gly	Thr	Leu	Gln	Ser	Ser
				245					250					255	
Pro	Ala	Thr	Thr	Pro	Ser	Gly	Ser	Leu	Ser	Gly	Ser	Gln	Asp	Asp	
		260					265						270		
Ser	Asp	Ser	Asp	Met	Thr	Phe	Ser	Val	Asn	Gln	Ser	Ser	Ser	Ala	Ser
		275					280					285			
Glu	Ser	Ser	Leu	Val	Thr	Ala	Pro	Ser	Ser	Pro	Leu	Ser	Pro	Pro	Val
	290					295					300				
Ser	Pro	Val	Phe	Ser	Pro	Pro	Glu	Pro	Ala	Gly	Ile	Lys	Asn	Gly	Glu
305					310					315					320
Cys	Thr	Val	Cys	Phe	Asp	Gly	Glu	Val	Asp	Thr	Val	Ile	Tyr	Thr	Cys
				325					330					335	

Gly His Met Cys Leu Cys His Ser Cys Gly Leu Arg Leu Lys Arg Gln  
340 345 350  
Ala Arg Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Val Ile  
355 360 365  
Lys Ile Tyr Arg Pro  
370

<210> 25  
<211> 955  
<212> DNA  
<213> Homo sapien

<400> 25  
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acccgccgt gctgcggccc cgccccgag cgacgcccg tcctgggcga ggcgccgcgc 120  
ttccacgcgc aggcctaaagg caagaacgtg cggctggacg gccactcgcg ccgggccaca 180  
cggcgcaaca gcttctgcaa tggcgtcacg ttcacgcagc ggcccatccg gctgtacgag 240  
caggtgcggc tgcgcctggt ggccgtgcgc cctggctgga gcggcgcgct gcgcttcggc 300  
ttcaccgcgc acgatccgtc gctcatgagc gcccaggaca tcccaagta cgcctgccc 360  
gacctggtca cgcggccggg ctactgggcc aaggcactgc ccgagaacct ggcgctgcgc 420  
gacacggtgc tggcctactg ggccgaccgc cacggccgcg tgttctacag cgtgaacgac 480  
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gatgtctacg gcatcaccga cgaggtgcag cttctgggta ccctgcagtc cagccctgcg 600  
accacgactc catcagggtc cctcagcggc tcccaggacg atagtgattc agatatgacc 660  
ttcagtgtca accagtcttc ctcggcatct gagtcatccc tggtgacggc cccagctcc 720  
ccgctgagcc ccccggtgtc ccccggtgtc tccccaccgg agccggcagg catcaagaat 780  
ggcgagtga cgggtgtgctt cgatggcgag gtggacacgg tcatctacac gtgtggacac 840  
atgtgcctgt gccacagctg cggcctgcgg ctcaagcgac aggcccgggc ctgctgcccc 900  
atctgccggc ggcccatcaa ggacgtcatt aagatctaca ggccatagcc tagcc 955

<210> 26  
<211> 315  
<212> PRT  
<213> Homo sapien

<400> 26  
Met Gly Asn Thr Val His Arg Thr Leu Pro Asp Pro Ser Pro Pro Ala  
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Arg Leu Leu Ala Thr Arg Pro Cys Cys Gly Pro Gly Pro Glu Arg Arg  
20 25 30  
Pro Val Leu Gly Glu Ala Pro Arg Phe His Ala Gln Ala Lys Gly Lys  
35 40 45  
Asn Val Arg Leu Asp Gly His Ser Arg Arg Ala Thr Arg Arg Asn Ser  
50 55 60  
Phe Cys Asn Gly Val Thr Phe Thr Gln Arg Pro Ile Arg Leu Tyr Glu  
65 70 75 80  
Gln Val Arg Leu Arg Leu Val Ala Val Arg Pro Gly Trp Ser Gly Ala  
85 90 95  
Leu Arg Phe Gly Phe Thr Ala His Asp Pro Ser Leu Met Ser Ala Gln  
100 105 110  
Asp Ile Pro Lys Tyr Ala Cys Pro Asp Leu Val Thr Arg Pro Gly Tyr  
115 120 125  
Trp Ala Lys Ala Leu Pro Glu Asn Leu Ala Leu Arg Asp Thr Val Leu  
130 135 140

Ala Tyr Trp Ala Asp Arg His Gly Arg Val Phe Tyr Ser Val Asn Asp  
145 150 155 160  
Gly Glu Pro Val Leu Phe His Cys Gly Val Ala Val Gly Gly Pro Leu  
165 170 175  
Trp Ala Leu Ile Asp Val Tyr Gly Ile Thr Asp Glu Val Gln Leu Leu  
180 185 190  
Gly Thr Leu Gln Ser Ser Pro Ala Thr Thr Thr Pro Ser Gly Ser Leu  
195 200 205  
Ser Gly Ser Gln Asp Asp Ser Asp Ser Asp Met Thr Phe Ser Val Asn  
210 215 220  
Gln Ser Ser Ser Ala Ser Glu Ser Ser Leu Val Thr Ala Pro Ser Ser  
225 230 235 240  
Pro Leu Ser Pro Pro Val Ser Pro Val Phe Ser Pro Pro Glu Pro Ala  
245 250 255  
Gly Ile Lys Asn Gly Glu Cys Thr Val Cys Phe Asp Gly Glu Val Asp  
260 265 270  
Thr Val Ile Tyr Thr Cys Gly His Met Cys Leu Cys His Ser Cys Gly  
275 280 285  
Leu Arg Leu Lys Arg Gln Ala Arg Ala Cys Cys Pro Ile Cys Arg Arg  
290 295 300  
Pro Ile Lys Asp Val Ile Lys Ile Tyr Arg Pro  
305 310 315

<210> 27

<211> 1641

<212> DNA

<213> Rat

<400> 27

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ttccacgcgc agccaaggg caagaacgtg cgtctagacg gtcactcgcg cagggccacg 180  
cgacggaaca gcttctgcaa cggagtcacc ttacgcagc ggccattcg cctgtacgag 240  
caggtgcggt tgcgcctggt ggctgtgcgt cctggctgga gcggcgcgct gcgcttcggc 300  
ttcactgcgc acgacccgtc gctcatgagc gcacaggata tcccaagta cgcctgcccc 360  
gacctggtca cagacctgg atactgggcc aaggcgtgc cggagaacct ggcgctgcgg 420  
gacacggtgc tggcctactg ggctgatcgt cacggctcgc tcttctatag tgtctatgat 480  
ggcgaaccag tgcgtgtcca ctgcggcgtg gccgtgggaa gccactctg ggcactcatc 540  
gacgtctatg gcatcacgga cgaggtgcag ctgctggaaa gcacctgcgc agacacgctg 600  
acccgctgc gcctgggcca ggccgcctc agcgcctgcc cgcctccggg cagccacgat 660  
gctgccaact tcgataataa cgagctggag aataaccagg tggtagcaa gctgggtcac 720  
ttggctctcg gccgtccgga cgcgcctgc cgtgcgtgg cccgcgaac gcgaggccc 780  
gcttcttcac ccgcgttgct ggacgtgag ctgcgtttcc acgccacgcg cggccccgac 840  
gtgagcctgt ttgcggaccg caggttagct tgcgcgcccc gcccgacgg cggccgcacg 900  
tttgtgttct ccgagcggcc gctgcggccc ggggagagcc tgtgcgtgga agtggggcgc 960  
ccggggctgg cggcgccgc agctgtggcc ttcggcatca cgtcctgcga tcctggcgcg 1020  
ctgcggccat ccgagctgcc cgcgatccc gctgcgtgc tggaccgcaa ggaatactgg 1080  
gtggtggcgc gcgcggggcc cgtgcccagc ggaggcgacg cactcagctt cacgctgcga 1140  
ccggcgcgcg acgtctgct ggcggtgaac gggcgccgc ggggacgctt gctgtgcgtg 1200  
gacacctcgc aggcgctctg gcccttcttc gctgtgcgcg gtggtgtggc gggtcagctg 1260  
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ggctctcagg atgacagcga ttccgacatg accttcgggg tcaaccagtc gtcacagca 1380  
tcagaatcgt ctctggtgac agccccagc tccccactga gtccccagc gtccccggcc 1440  
ttctctgcac ccgagccggc cggcagcagg aatggagagt gcacggtgtg cttcgacagc 1500





355                      360                      365  
 Pro Ser Gly Gly Asp Ala Leu Ser Phe Thr Leu Arg Pro Gly Gly Asp  
 370                      375                      380  
 Val Leu Leu Ala Val Asn Gly Arg Pro Arg Gly Arg Leu Leu Cys Val  
 385                      390                      395                      400  
 Asp Thr Ser Gln Ala Leu Trp Ala Phe Phe Ala Val Arg Gly Gly Val  
 405                      410                      415  
 Ala Gly Gln Leu Arg Leu Leu Gly Thr Val Gln Ser Gly Pro Glu Ala  
 420                      425                      430  
 Thr Thr Pro Ser Gly Ser Phe Ser Gly Ser Gln Asp Asp Ser Asp Ser  
 435                      440                      445  
 Asp Met Thr Phe Gly Val Asn Gln Ser Ser Ser Ala Ser Glu Ser Ser  
 450                      455                      460  
 Leu Val Thr Ala Pro Ser Ser Pro Leu Ser Pro Pro Val Ser Pro Ala  
 465                      470                      475                      480  
 Phe Ser Ala Pro Glu Pro Ala Gly Ser Arg Asn Gly Glu Cys Thr Val  
 485                      490                      495  
 Cys Phe Asp Ser Glu Val Asp Thr Val Ile Tyr Thr Cys Gly His Met  
 500                      505                      510  
 Cys Leu Cys His Ser Cys Arg Leu Arg Leu Arg Lys Gln Ala Arg Ala  
 515                      520                      525  
 Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Val Ile Lys Ile Tyr  
 530                      535                      540  
 Arg Pro  
 545

<210> 29  
 <211> 789  
 <212> DNA  
 <213> Homo sapien

<400> 29  
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 cgcaccacgt tccacgacgg catcgtgttc agccagcggc cggcgcgctt gggcgagcgt 180  
 gtggcgctgc gactgctgcg ggaggagagc ggctggtgcg gcggcctccg cgtgggcttc 240  
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 ctggaggagc agagcccgcg gtgggcggcc gtgctgcctg agggctgcgc gctcactggg 360  
 gacttggtcc gcttctgggt ggaccgcgcg ggctgcctct tcgccaaggc caacgccggc 420  
 tgccggctcc tgctgcgtga gggcgtgccc gtcggcgccc cgctctgggc cgtgatggac 480  
 gtgtatggga ccactaaggc catcgagctg ctggatccca cagccagccg gctcccaaca 540  
 cccatgccat gggacctcag caacaaggct gtgcctgagc ccaaagccac accaggagag 600  
 gactgtgcca tctgcttcta tcacgctgcc aacaccgcgc ttgtgccctg cggccacaca 660  
 tacttctgca gatactgtgc ctggcggtgc ttcagcgata cggccaagtg ccctgtgtgc 720  
 cgctggcaga tagaggcggc agcccctgcg cagggccctc ctgctctgag gggtgaggaa 780  
 ggctcatga 789

<210> 30  
 <211> 262  
 <212> PRT  
 <213> Homo sapien

<400> 30  
 Met Gly Ala Gln Leu Cys Phe Glu Ala Asn Ala Lys Ala Pro Arg Glu

1 5 10 15  
 Ala Leu Arg Phe His Ala Glu Ala Lys Gly Ala Gln Val Arg Leu Asp  
 20 25 30  
 Thr Arg Gly Cys Ile Ala His Arg Arg Thr Thr Phe His Asp Gly Ile  
 35 40 45  
 Val Phe Ser Gln Arg Pro Val Arg Leu Gly Glu Arg Val Ala Leu Arg  
 50 55 60  
 Val Leu Arg Glu Glu Ser Gly Trp Cys Gly Gly Leu Arg Val Gly Phe  
 65 70 75 80  
 Thr Arg Leu Asp Pro Ala Cys Val Ser Val Pro Ser Leu Pro Pro Phe  
 85 90 95  
 Leu Cys Pro Asp Leu Glu Glu Gln Ser Pro Thr Trp Ala Ala Val Leu  
 100 105 110  
 Pro Glu Gly Cys Ala Leu Thr Gly Asp Leu Val Arg Phe Trp Val Asp  
 115 120 125  
 Arg Arg Gly Cys Leu Phe Ala Lys Val Asn Ala Gly Cys Arg Leu Leu  
 130 135 140  
 Leu Arg Glu Gly Val Pro Val Gly Ala Pro Leu Trp Ala Val Met Asp  
 145 150 155 160  
 Val Tyr Gly Thr Thr Lys Ala Ile Glu Leu Leu Asp Pro Thr Ala Ser  
 165 170 175  
 Arg Leu Pro Thr Pro Met Pro Trp Asp Leu Ser Asn Lys Ala Val Pro  
 180 185 190  
 Glu Pro Lys Ala Thr Pro Gly Glu Cys Ala Ile Cys Phe Tyr His  
 195 200 205  
 Ala Ala Asn Thr Arg Leu Val Pro Cys Gly His Thr Tyr Phe Cys Arg  
 210 215 220  
 Tyr Cys Ala Trp Arg Val Phe Ser Asp Thr Ala Lys Cys Pro Val Cys  
 225 230 235 240  
 Arg Trp Gln Ile Glu Ala Val Ala Pro Ala Gln Gly Pro Pro Ala Leu  
 245 250 255  
 Arg Val Glu Glu Gly Ser  
 260

<210> 31

<211> 765

<212> DNA

<213> mouse

<400> 31

atgggttctc tcctcagccc tgaggccaat gccgaggtgc cccgcgaggc ccttagtttc 60  
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 cgctcgacgt tccacgatgg tatcgtgttc agccagaggc cggctctggc gggtagcgt 180  
 gttgctctgc gcgtcctgca acatgaagaa ggctgggtgc gtggcctccg cgtgggcttc 240  
 acgcgcctgg accctgcgca agtggccgca tcctgcctgc cacccttcgt gtgcccggac 300  
 ctggaggagc agagtccac gtgggcagcg ttgcttcagc agggcttcgt tcgtgcgggg 360  
 aatgtgggtc gcttctgggt gaaccgtaga ggggtggctc tcgccaaggc caacgctggc 420  
 cgccccctct tgctgcgcaa agacgtgctg gtccagggag ccccgctctg ggcggtgatg 480  
 gatgtgtacg ggaccacgaa agccattgag cttctggatc ccaaagccaa cgcctggatt 540  
 cgtagtggtg agcctgtgcc agagtctgaa gtcatatcag gagaggagtg tgtcatctgc 600  
 ttccacaaca ctgccaacac ccgcctcatg ccctgtggcc actcacactt ctgtggctcc 660  
 tgtgcctggc acatcttcaa agacacggcc aggtgccccca tatgtcgctg gcagatcgag 720  
 gaggtggctg tagtgtcttc actgaaggct gaggaaggct cctga 765

<210> 32  
 <211> 254  
 <212> PRT  
 <213> mouse

<400> 32  
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 Ala Leu Ser Phe His Gly Asn Ala Thr Gly Ala Gln Val His Leu Asp  
 20 25 30  
 Asp Gln Arg Ser Thr Ala Arg Arg Arg Ser Thr Phe His Asp Gly Ile  
 35 40 45  
 Val Phe Ser Gln Arg Pro Val Trp Pro Gly Glu Arg Val Ala Leu Arg  
 50 55 60  
 Val Leu Arg His Glu Glu Gly Trp Cys Gly Gly Leu Arg Val Gly Phe  
 65 70 75 80  
 Thr Arg Leu Asp Pro Ala Gln Val Ala Ala Ser Cys Leu Pro Pro Phe  
 85 90 95  
 Val Cys Pro Asp Leu Glu Glu Gln Ser Pro Thr Trp Ala Ala Leu Leu  
 100 105 110  
 Pro Glu Gly Phe Val Arg Ala Gly Asn Val Val Cys Phe Trp Val Asn  
 115 120 125  
 Arg Arg Gly Trp Leu Phe Ala Lys Val Asn Ala Gly Arg Pro Leu Leu  
 130 135 140  
 Leu Arg Lys Asp Val Leu Val Gln Gly Ala Pro Leu Trp Ala Val Met  
 145 150 155 160  
 Asp Val Tyr Gly Thr Thr Lys Ala Ile Glu Leu Leu Asp Pro Lys Ala  
 165 170 175  
 Asn Ala Trp Ile Arg Ser Gly Glu Pro Val Pro Glu Ser Glu Val Ile  
 180 185 190  
 Ser Gly Glu Glu Cys Val Ile Cys Phe His Asn Thr Ala Asn Thr Arg  
 195 200 205  
 Leu Met Pro Cys Gly His Ser His Phe Cys Gly Ser Cys Ala Trp His  
 210 215 220  
 Ile Phe Lys Asp Thr Ala Arg Cys Pro Ile Cys Arg Trp Gln Ile Glu  
 225 230 235 240  
 Glu Val Ala Val Val Ser Ser Leu Lys Ala Glu Glu Gly Ser  
 245 250

<210> 33  
 <211> 250  
 <212> DNA  
 <213> Homo sapien

<400> 33  
 cgcttccatc ggggtgcacgg tgccaacatc cgcgtggacc cctctgggac gcggggccaca 60  
 cgcgtggaga gcttcgcca cggcgtgtgc ttcagccgcg agccgctggc cccggggccag 120  
 gtcttcctgg tcgagatcga ggagaaagag ctgggctggg gcggacatct gcgtctcggg 180  
 ctgaccgcgc tggacccgc cagtctggcc cccgttcccg agttttctct gcccgatctg 240  
 gtcaacctgg 250

<210> 34  
 <211> 83  
 <212> PRT

<213> Homo sapien

<400> 34

Arg Phe His Arg Val His Gly Ala Asn Ile Arg Val Asp Pro Ser Gly  
1 5 10 15  
Thr Arg Ala Thr Arg Val Glu Ser Phe Ala His Gly Val Cys Phe Ser  
20 25 30  
Arg Glu Pro Leu Ala Pro Gly Gln Val Phe Leu Val Glu Ile Glu Glu  
35 40 45  
Lys Glu Leu Gly Trp Cys Gly His Leu Arg Leu Gly Leu Thr Ala Leu  
50 55 60  
Asp Pro Ala Ser Leu Ala Pro Val Pro Glu Phe Ser Leu Pro Asp Leu  
65 70 75 80  
Val Asn Leu

<210> 35

<211> 1743

<212> DNA

<213> rat

<400> 35

atggcggatt tgcaggagtt gaggaatatg gtttctagtt ttaggggttc tgaattacaa 60  
gtgttactgg gctttgctgg acggaataaa agtgggcgca agcatgacct cctgatgagg 120  
gcgttgcaatt tactgaagag tggctgcagc cctgcgggtc agattaaaat tgcagaatta 180  
tacagacgcc gataccacg gacacttgaa ggactttctg atctatccac aatcaaattct 240  
tcagttttca gtttgatgg tagctcatca ccagtagagc ctgacttggc cgtggctggg 300  
atccactcgt tgccttctac ttccattgca cctcattcac cgtcatctcc tgcgcttct 360  
gtgctgcttc aagacactaa gccacggtt gagatgcagc aaccatctcc tcccattcct 420  
cctgtccatt ctgacgtgca gttaaaaacg ctgcccttct atgacgtcct tgatgttctc 480  
atcaagccca caagtttagt tcaaagcagt attcagcggg ttcaagagaa gttttttatt 540  
tttgctttga caccacagca agttagagag atatgcattt caagggattt tttgccaggg 600  
ggcaggagag actacacagt ccaagtcag ctgcgacttt gcttggcaga gaccagttgc 660  
cctcaagaag ataactatcc caatagtttg tgtataaaag taaatgggaa actctttcct 720  
ttgcctggct atgcaccacc acctaaaaat gggatcgaa agaagcgtcc tggacgcccc 780  
ctgaatatta catctttagt gagattgtct tcagctgtgc caaatcagat ttctatttct 840  
tgggcatctg aaattggaaa gaattactcc atgtctgtgt atcttgtacg acagcttaca 900  
tcagccatgt tattacagag attaaaaatg aaaggtatta gaaatcctga tcattccaaa 960  
gcactcatta aagaaaaact tactgcagat cctgatagtg aaattgctac aactagtctt 1020  
cgagtgtcct tgatgtgccc tttaggaaaa atgaggctga caatcccgtg ccgcgcagtg 1080  
acgtgtacac atctgcagtg ctttgatgct gccctgtatc ttcagatgaa tgagaagaag 1140  
cccacctgga tttgtcctgt ttgtgacaaa aaggctgcct atgagagtct gatactagat 1200  
gggcttttta tggaaattct caatgactgt tctgatgtgg atgagatcaa attccaggaa 1260  
gatggttcct ggtgccccat gagacctaag aaagaagcta tgaaagtaac cagccagccc 1320  
tgtacaaaag tagaaagttc aagtgtcttt agtaaaccct gttcagtgcac tgtagccagt 1380  
gatgcaagca agaagaagat tgatgttatt gatctaacaa tagagagctc ttctgatgaa 1440  
gaggaagacc ctcccgccaa aaggaaatgc atctttatgt cagaaacaca aagcagtcca 1500  
accaaagggg ttctcatgta tcagccatct tctgtaaggg tgcccagtgt gacttcagtt 1560  
gatcctgctg ctattccacc ttcatlaaca gactactcag taccattcca ccacagcca 1620  
gtgtcgagca tgtcatcaga tttgccaggg ttggattttc tttcccttat tccagttgat 1680  
cccagctctc acctcaccct taacagcaag cagtacgtct gtcaccacca ccagcccca 1740  
tga 1743

<210> 36

<211> 580

<212> PRT

<213> rat

<400> 36

Met Ala Asp Phe Glu Glu Leu Arg Asn Met Val Ser Ser Phe Arg Val  
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Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly Arg Asn Lys Ser Gly  
20 25 30  
Arg Lys His Asp Leu Leu Met Arg Ala Leu His Leu Leu Lys Ser Gly  
35 40 45  
Cys Ser Pro Ala Val Gln Ile Lys Ile Arg Glu Leu Tyr Arg Arg Arg  
50 55 60  
Tyr Pro Arg Thr Leu Glu Gly Leu Ser Asp Leu Ser Thr Ile Lys Ser  
65 70 75 80  
Ser Val Phe Ser Leu Asp Gly Ser Ser Ser Pro Val Glu Pro Asp Leu  
85 90 95  
Ala Val Ala Gly Ile His Ser Leu Pro Ser Thr Ser Ile Ala Pro His  
100 105 110  
Ser Pro Ser Ser Pro Val Ala Ser Val Leu Leu Gln Asp Thr Lys Pro  
115 120 125  
Thr Phe Glu Met Gln Gln Pro Ser Pro Pro Ile Pro Pro Val His Pro  
130 135 140  
Asp Val Gln Leu Lys Thr Leu Pro Phe Tyr Asp Val Leu Asp Val Leu  
145 150 155 160  
Ile Lys Pro Thr Ser Leu Val Gln Ser Ser Ile Gln Arg Phe Gln Glu  
165 170 175  
Lys Phe Phe Ile Phe Ala Leu Thr Pro Gln Gln Val Arg Glu Ile Cys  
180 185 190  
Ile Ser Arg Asp Phe Leu Pro Gly Gly Arg Arg Asp Tyr Thr Val Gln  
195 200 205  
Val Gln Leu Arg Leu Cys Leu Ala Glu Thr Ser Cys Pro Gln Glu Asp  
210 215 220  
Asn Tyr Pro Asn Ser Leu Cys Ile Lys Val Asn Gly Lys Leu Phe Pro  
225 230 235 240  
Leu Pro Gly Tyr Ala Pro Pro Pro Lys Asn Gly Ile Glu Gln Lys Arg  
245 250 255  
Pro Gly Arg Pro Leu Asn Ile Thr Ser Leu Val Arg Leu Ser Ser Ala  
260 265 270  
Val Pro Asn Gln Ile Ser Ile Ser Trp Ala Ser Glu Ile Gly Lys Asn  
275 280 285  
Tyr Ser Met Ser Val Tyr Leu Val Arg Gln Leu Thr Ser Ala Met Leu  
290 295 300  
Leu Gln Arg Leu Lys Met Lys Gly Ile Arg Asn Pro Asp His Ser Lys  
305 310 315 320  
Ala Leu Ile Lys Glu Lys Leu Thr Ala Asp Pro Asp Ser Glu Ile Ala  
325 330 335  
Thr Thr Ser Leu Arg Val Ser Leu Met Cys Pro Leu Gly Lys Met Arg  
340 345 350  
Leu Thr Ile Pro Cys Arg Ala Val Thr Cys Thr His Leu Gln Cys Phe  
355 360 365  
Asp Ala Ala Leu Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Ile  
370 375 380  
Cys Pro Val Cys Asp Lys Lys Ala Ala Tyr Glu Ser Leu Ile Leu Asp  
385 390 395 400

Gly Leu Phe Met Glu Ile Leu Asn Asp Cys Ser Asp Val Asp Glu Ile  
 405 410 415  
 Lys Phe Gln Glu Asp Gly Ser Trp Cys Pro Met Arg Pro Lys Lys Glu  
 420 425 430  
 Ala Met Lys Val Thr Ser Gln Pro Cys Thr Lys Val Glu Ser Ser Ser  
 435 440 445  
 Val Phe Ser Lys Pro Cys Ser Val Thr Val Ala Ser Asp Ala Ser Lys  
 450 455 460  
 Lys Lys Ile Asp Val Ile Asp Leu Thr Ile Glu Ser Ser Ser Asp Glu  
 465 470 475 480  
 Glu Glu Asp Pro Pro Ala Lys Arg Lys Cys Ile Phe Met Ser Glu Thr  
 485 490 495  
 Gln Ser Ser Pro Thr Lys Gly Val Leu Met Tyr Gln Pro Ser Ser Val  
 500 505 510  
 Arg Val Pro Ser Val Thr Ser Val Asp Pro Ala Ala Ile Pro Pro Ser  
 515 520 525  
 Leu Thr Asp Tyr Ser Val Pro Phe His His Thr Pro Val Ser Ser Met  
 530 535 540  
 Ser Ser Asp Leu Pro Gly Leu Asp Phe Leu Ser Leu Ile Pro Val Asp  
 545 550 555 560  
 Pro Gln Ser His Leu Thr Leu Asn Ser Lys Gln Tyr Val Cys His His  
 565 570 575  
 His Gln Pro Pro  
 580

<210> 37  
 <211> 1251  
 <212> DNA  
 <213> Homo sapien

<400> 37  
 atgagcacca agcagatcac ttgcaggtat tttatgcatg gtgtgtgtcg ggaaggaagt 60  
 cagtgcctat tctcacatga cttggcaaac agcaaacctg ccaccatctg caagtactac 120  
 cagaagggct actgtgccta tggaactcgg tgcatgatg accacacgag gccctctgct 180  
 gcagctggag gtgctgtggg caccatggcc cacagtgtgc cctccccagc tttccacagt 240  
 cctcaccctc cttccgaggt cactgcatcc attgtgaaaa ctaactcaca tgaacccgga 300  
 aagcgtgaaa agagaacatt ggttcttaga gaccgaaatc tctctggcat ggctgaaagg 360  
 aagaccagc cgagcatggg gagtaatcca ggcagctgca gcgaccccca gccagcccc 420  
 gagatgaagc cgcattccta cctggatgcc atcaggagtg gccttgatga cgtggaggcc 480  
 agcagctcct acagcaacga gcagcagctg tgcccctacg cagctgctgg ggagtgccgg 540  
 tttggggatg cctgtgtcta cctgcacggg gaggtgtgtg aaatctgtag gctgcaagtc 600  
 ttgcacccat tgcacccaga gcagaggaag gctcatgaaa agatctgcat gttgacgttc 660  
 gaacacgaga tggaaaaggc ctttgccttc caggcaagcc aggacaaaagt gtgcagtatc 720  
 tgcattggaag tgatcctgga gaaggcctct gcttctgaga ggagatttgg gattctctcc 780  
 aattgcaatc acacgtactg tttgtcctgc atccggcagt ggcgggtgtgc cgaacagttt 840  
 gaaaacccaa tcattaagtc ttgtccagaa tgccgtgtga tatcagagtt tgtaattcca 900  
 agtgtgtatt ggggtggaaga tcagaataaaa aagaacgagt tgattgaagc tttcaaacag 960  
 gggatgggga aaaaagcctg taaatacttt gagcaaggca aggggacctg ccatttggga 1020  
 agcaaatgct tttatcgcca tggttacctc gatgggcggc tagcagagcc tgagaaacct 1080  
 cggaacagc tcatgtctca aggcactgtg aggttcttta attcagtgcg gctctgggat 1140  
 ttcacgaga accgagaaag ccggcatgtc cccaacaatg aagatgtcga catgacagag 1200  
 ctcggggacc tcttcatgca cctttctgga gtggaatcat cagaacccta a 1251

<210> 38

<211> 416  
 <212> PRT  
 <213> Homo sapien

<400> 38

Met	Ser	Thr	Lys	Gln	Ile	Thr	Cys	Arg	Tyr	Phe	Met	His	Gly	Val	Cys
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Arg	Glu	Gly	Ser	Gln	Cys	Leu	Phe	Ser	His	Asp	Leu	Ala	Asn	Ser	Lys
			20					25					30		
Pro	Ser	Thr	Ile	Cys	Lys	Tyr	Tyr	Gln	Lys	Gly	Tyr	Cys	Ala	Tyr	Gly
		35					40					45			
Thr	Arg	Cys	Arg	Tyr	Asp	His	Thr	Arg	Pro	Ser	Ala	Ala	Ala	Gly	Gly
	50					55					60				
Ala	Val	Gly	Thr	Met	Ala	His	Ser	Val	Pro	Ser	Pro	Ala	Phe	His	Ser
65					70					75					80
Pro	His	Pro	Pro	Ser	Glu	Val	Thr	Ala	Ser	Ile	Val	Lys	Thr	Asn	Ser
				85					90					95	
His	Glu	Pro	Gly	Lys	Arg	Glu	Lys	Arg	Thr	Leu	Val	Leu	Arg	Asp	Arg
			100					105					110		
Asn	Leu	Ser	Gly	Met	Ala	Glu	Arg	Lys	Thr	Gln	Pro	Ser	Met	Val	Ser
		115					120					125			
Asn	Pro	Gly	Ser	Cys	Ser	Asp	Pro	Gln	Pro	Ser	Pro	Glu	Met	Lys	Pro
	130					135					140				
His	Ser	Tyr	Leu	Asp	Ala	Ile	Arg	Ser	Gly	Leu	Asp	Asp	Val	Glu	Ala
145					150					155					160
Ser	Ser	Ser	Tyr	Ser	Asn	Glu	Gln	Gln	Leu	Cys	Pro	Tyr	Ala	Ala	Ala
				165					170					175	
Gly	Glu	Cys	Arg	Phe	Gly	Asp	Ala	Cys	Val	Tyr	Leu	His	Gly	Glu	Val
			180					185					190		
Cys	Glu	Ile	Cys	Arg	Leu	Gln	Val	Leu	His	Pro	Phe	Asp	Pro	Glu	Gln
		195					200					205			
Arg	Lys	Ala	His	Glu	Lys	Ile	Cys	Met	Leu	Thr	Phe	Glu	His	Glu	Met
	210					215					220				
Glu	Lys	Ala	Phe	Ala	Phe	Gln	Ala	Ser	Gln	Asp	Lys	Val	Cys	Ser	Ile
225					230					235					240
Cys	Met	Glu	Val	Ile	Leu	Glu	Lys	Ala	Ser	Ala	Ser	Glu	Arg	Arg	Phe
				245					250					255	
Gly	Ile	Leu	Ser	Asn	Cys	Asn	His	Thr	Tyr	Cys	Leu	Ser	Cys	Ile	Arg
		260						265					270		
Gln	Trp	Arg	Cys	Ala	Glu	Gln	Phe	Glu	Asn	Pro	Ile	Ile	Lys	Ser	Cys
	275						280						285		
Pro	Glu	Cys	Arg	Val	Ile	Ser	Glu	Phe	Val	Ile	Pro	Ser	Val	Tyr	Trp
	290					295					300				
Val	Glu	Asp	Gln	Asn	Lys	Lys	Asn	Glu	Leu	Ile	Glu	Ala	Phe	Lys	Gln
305					310					315					320
Gly	Met	Gly	Lys	Lys	Ala	Cys	Lys	Tyr	Phe	Glu	Gln	Gly	Lys	Gly	Thr
				325					330					335	
Cys	Pro	Phe	Gly	Ser	Lys	Cys	Leu	Tyr	Arg	His	Ala	Tyr	Pro	Asp	Gly
		340						345					350		
Arg	Leu	Ala	Glu	Pro	Glu	Lys	Pro	Arg	Lys	Gln	Leu	Ser	Ser	Gln	Gly
		355					360					365			
Thr	Val	Arg	Phe	Phe	Asn	Ser	Val	Arg	Leu	Trp	Asp	Phe	Ile	Glu	Asn
	370					375					380				
Arg	Glu	Ser	Arg	His	Val	Pro	Asn	Asn	Glu	Asp	Val	Asp	Met	Thr	Glu
385					390					395					400

Leu Gly Asp Leu Phe Met His Leu Ser Gly Val Glu Ser Ser Glu Pro  
 405 410 415

<210> 39  
 <211> 738  
 <212> DNA  
 <213> Homo sapien

<400> 39  
 atgaaacgga ggaagcaaga tgaagggcag agggaaggct cctgcatggc tgaggatgat 60  
 gctgtggaca tcgagcatga gaacaacaac cgctttgagg agtatgagt gtgtggacag 120  
 aagcggatac gggccaccac tctcctggaa ggtggcttcc gaggctctgg cttcatcatg 180  
 tgcagcggca aagagaaccc ggacagtgat gctgacttgg atgtggatgg ggatgacact 240  
 ctggagtatg ggaagccaca atacacagag gctgatgtca tcccctgcac aggcgaggag 300  
 cctggtgaag ccaaggagag agaggcactt cggggcgcag tcctaaatgg cggccctccc 360  
 agcacgcgca tcacacctga gttctctaaa tgggccagtg atgagatgcc atccaccagc 420  
 aatggtgaaa gcagcaagca ggaggccatg cagaagacct gcaagaacag cgacatcgag 480  
 aaaatcaccg aagattcagc tgtgaccacg tttgaggctc tgaaggctcg ggtcagagaa 540  
 cttgaacggc agctatctcg tggggaccgt tacaaatgcc tcatctgcat ggactcgtac 600  
 tcgatgcccc taacgtccat ccagtgttgg cacgtgcact gcgaggagt ctggctgcgg 660  
 accctgggtg ccaagaagct ctgccctcag tgcaacacga tcacagcgcc cggagacctg 720  
 cggaggatct acttgtga 738

<210> 40  
 <211> 245  
 <212> PRT  
 <213> Homo sapien

<400> 40  
 Met Lys Arg Arg Lys Gln Asp Glu Gly Gln Arg Glu Gly Ser Cys Met  
 1 5 10 15  
 Ala Glu Asp Asp Ala Val Asp Ile Glu His Glu Asn Asn Asn Arg Phe  
 20 25 30  
 Glu Glu Tyr Glu Trp Cys Gly Gln Lys Arg Ile Arg Ala Thr Thr Leu  
 35 40 45  
 Leu Glu Gly Gly Phe Arg Gly Ser Gly Phe Ile Met Cys Ser Gly Lys  
 50 55 60  
 Glu Asn Pro Asp Ser Asp Ala Asp Leu Asp Val Asp Gly Asp Asp Thr  
 65 70 75 80  
 Leu Glu Tyr Gly Lys Pro Gln Tyr Thr Glu Ala Asp Val Ile Pro Cys  
 85 90 95  
 Thr Gly Glu Glu Pro Gly Glu Ala Lys Glu Arg Glu Ala Leu Arg Gly  
 100 105 110  
 Ala Val Leu Asn Gly Gly Pro Pro Ser Thr Arg Ile Thr Pro Glu Phe  
 115 120 125  
 Ser Lys Trp Ala Ser Asp Glu Met Pro Ser Thr Ser Asn Gly Glu Ser  
 130 135 140  
 Ser Lys Gln Glu Ala Met Gln Lys Thr Cys Lys Asn Ser Asp Ile Glu  
 145 150 155 160  
 Lys Ile Thr Glu Asp Ser Ala Val Thr Thr Phe Glu Ala Leu Lys Ala  
 165 170 175  
 Arg Val Arg Glu Leu Glu Arg Gln Leu Ser Arg Gly Asp Arg Tyr Lys  
 180 185 190  
 Cys Leu Ile Cys Met Asp Ser Tyr Ser Met Pro Leu Thr Ser Ile Gln



195                      200                      205  
 Cys Trp His Val His Cys Glu Glu Cys Trp Leu Arg Thr Leu Gly Ala  
 210                      215                      220  
 Lys Lys Leu Cys Pro Gln Cys Asn Thr Ile Thr Ala Pro Gly Asp Leu  
 225                      230                      235                      240  
 Arg Arg Ile Tyr Leu  
 245

<210> 41  
 <211> 1425  
 <212> DNA  
 <213> Homo sapien

<400> 41  
 atgtcgtcag aagatcgaga agctcaggag gatgaattgc tggccctggc aagtattttac 60  
 gatggagatg aatttagaaa agcagagtct gtccaagggt gagaaaccag gatctattttg 120  
 gatttgccac agaatttcaa gatattttgt agcggcaatt caaatgagtg tctccagaat 180  
 agtggctttg aatacaccat ttgctttctg cctccacttg tgctgaactt tgaactgcca 240  
 ccagattatc catcctcttc cccaccttca ttcacactta gtggcaaagt gctgtcacca 300  
 actcagctat ctgctctatg caagcactta gacaacctat gggaagaaca ccgtggcagc 360  
 gtggctcctgt ttgcctggat gcaatttctt aaggaagaga ccctagcata cttgaatatt 420  
 gtctctcctt ttgagctcaa gattggttct cagaaaaaag tgcagagaag gacagctcaa 480  
 gcttctccca acacagagct agattttgga ggagctgctg gatctgatgt agaccaagag 540  
 gaaatttggt atgagagagc agtgcaggat gtggaatcac tgtcaaactc gatccaggaa 600  
 atcttggaact ttgatcaagc tcagcagata aaatgcttta atagtaaatt gttcctgtgc 660  
 agtatctggt tctgtgagaa gctgggtagt gaatgcatgt acttcttgga gtgcaggcat 720  
 gtgtactgca aagcctgtct gaaggactac tttgaaatcc agatcagaga tggccagggt 780  
 caatgcctca actgcccaga accaaagtgc ccttcggtgg ccactcctgg tcaggtcaaa 840  
 gagttagtgg aagcagagtt atttgcccgt tatgaccgcc ttctcctcca gtcctccttg 900  
 gacctgatgg cagatgtggt gtactgcccc cggccgtgct gccagctgcc tgtgatgcag 960  
 gaacctgggt gcacctgggt tatctgctcc agctgcaatt ttgccttctg tactttgtgc 1020  
 aggttgacct accatggggt ctccccatgt aaggtgactg cagagaaatt aatggactta 1080  
 cgaaatgaat acctgcaagc ggatgaggct aataaaaagac ttttggatca aaggtatggt 1140  
 aagagagtga ttcagaaggc actggaagag atggaaaagta aggagtggct agagaagaac 1200  
 tcaaagagct gccatgttg tggaaactccc atagagaaat tagacggatg taacaagatg 1260  
 acatgtactg gctgtatgca atatttctgt tggatttgca tgggttctct ctctagagca 1320  
 aacccttaca aacatttcaa tgaccctggt tcaccatggt ttaaccggct gttttatgct 1380  
 gtggatgttg acgacgatat ttgggaagat gaggtagaag actag 1425

<210> 42  
 <211> 474  
 <212> PRT  
 <213> Homo sapien

<400> 42  
 Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu  
 1                      5                      10                      15  
 Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln  
 20                      25                      30  
 Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile  
 35                      40                      45  
 Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu  
 50                      55                      60  
 Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro

65	Pro	Asp	Tyr	Pro	Ser	Ser	Ser	Pro	Pro	Ser	Phe	Thr	Leu	Ser	Gly	Lys	80
					85					90					95		
Trp	Leu	Ser	Pro	Thr	Gln	Leu	Ser	Ala	Leu	Cys	Lys	His	Leu	Asp	Asn		
			100					105					110				
Leu	Trp	Glu	Glu	His	Arg	Gly	Ser	Val	Val	Leu	Phe	Ala	Trp	Met	Gln		
		115					120					125					
Phe	Leu	Lys	Glu	Glu	Thr	Leu	Ala	Tyr	Leu	Asn	Ile	Val	Ser	Pro	Phe		
		130				135					140						
Glu	Leu	Lys	Ile	Gly	Ser	Gln	Lys	Lys	Val	Gln	Arg	Arg	Thr	Ala	Gln		
145					150					155					160		
Ala	Ser	Pro	Asn	Thr	Glu	Leu	Asp	Phe	Gly	Gly	Ala	Ala	Gly	Ser	Asp		
			165						170					175			
Val	Asp	Gln	Glu	Glu	Ile	Val	Asp	Glu	Arg	Ala	Val	Gln	Asp	Val	Glu		
		180						185					190				
Ser	Leu	Ser	Asn	Leu	Ile	Gln	Glu	Ile	Leu	Asp	Phe	Asp	Gln	Ala	Gln		
		195					200					205					
Gln	Ile	Lys	Cys	Phe	Asn	Ser	Lys	Leu	Phe	Leu	Cys	Ser	Ile	Cys	Phe		
	210					215					220						
Cys	Glu	Lys	Leu	Gly	Ser	Glu	Cys	Met	Tyr	Phe	Leu	Glu	Cys	Arg	His		
225					230					235					240		
Val	Tyr	Cys	Lys	Ala	Cys	Leu	Lys	Asp	Tyr	Phe	Glu	Ile	Gln	Ile	Arg		
			245						250					255			
Asp	Gly	Gln	Val	Gln	Cys	Leu	Asn	Cys	Pro	Glu	Pro	Lys	Cys	Pro	Ser		
		260						265					270				
Val	Ala	Thr	Pro	Gly	Gln	Val	Lys	Glu	Leu	Val	Glu	Ala	Glu	Leu	Phe		
		275					280					285					
Ala	Arg	Tyr	Asp	Arg	Leu	Leu	Leu	Gln	Ser	Ser	Leu	Asp	Leu	Met	Ala		
	290					295					300						
Asp	Val	Val	Tyr	Cys	Pro	Arg	Pro	Cys	Cys	Gln	Leu	Pro	Val	Met	Gln		
305					310					315					320		
Glu	Pro	Gly	Cys	Thr	Met	Gly	Ile	Cys	Ser	Ser	Cys	Asn	Phe	Ala	Phe		
			325						330					335			
Cys	Thr	Leu	Cys	Arg	Leu	Thr	Tyr	His	Gly	Val	Ser	Pro	Cys	Lys	Val		
		340						345					350				
Thr	Ala	Glu	Lys	Leu	Met	Asp	Leu	Arg	Asn	Glu	Tyr	Leu	Gln	Ala	Asp		
		355					360					365					
Glu	Ala	Asn	Lys	Arg	Leu	Leu	Asp	Gln	Arg	Tyr	Gly	Lys	Arg	Val	Ile		
	370					375					380						
Gln	Lys	Ala	Leu	Glu	Glu	Met	Glu	Ser	Lys	Glu	Trp	Leu	Glu	Lys	Asn		
385					390					395					400		
Ser	Lys	Ser	Cys	Pro	Cys	Cys	Gly	Thr	Pro	Ile	Glu	Lys	Leu	Asp	Gly		
			405						410					415			
Cys	Asn	Lys	Met	Thr	Cys	Thr	Gly	Cys	Met	Gln	Tyr	Phe	Cys	Trp	Ile		
		420						425					430				
Cys	Met	Gly	Ser	Leu	Ser	Arg	Ala	Asn	Pro	Tyr	Lys	His	Phe	Asn	Asp		
	435						440					445					
Pro	Gly	Ser	Pro	Cys	Phe	Asn	Arg	Leu	Phe	Tyr	Ala	Val	Asp	Val	Asp		
	450					455					460						
Asp	Asp	Ile	Trp	Glu	Asp	Glu	Val	Glu	Asp								
465					470												

<210> 43

<211> 6

<212> PRT  
<213> Artificial Sequence

<220>  
<223> nuclear localization signal

<400> 43  
His Lys Ala Val Lys Arg  
1 5

<210> 44  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> nuclear localization signal

<400> 44  
Arg Leu Lys Ile Thr Lys Lys  
1 5

<210> 45  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> putative protein kinase phosphorylation site

<400> 45  
Arg Pro Arg Ser Phe Thr  
1 5

<210> 46  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> protein kinase phosphorylation site consensus  
sequence

<221> VARIANT  
<222> 2, 4, 5  
<223> Xaa = any amino acid

<400> 46  
Arg Xaa Arg Xaa Xaa Ser Thr  
1 5

<210> 47  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<221> VARIANT  
<222> 3, 5, 8, 10, 12, 15, 16, 17, 19, 20, 21, 22  
<223> Xaa = any amino acid

<400> 47  
Ser Thr Xaa Pro Xaa Ser Pro Xaa Ser Xaa Pro Xaa Ser Pro Xaa Xaa  
1 5 10 15  
Xaa Gly Xaa Xaa Xaa Xaa Ser Asp  
20

<210> 48  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> neuralized homology repeat domain

<400> 48  
Leu Pro Lys Tyr Ala Cys Pro Asp Leu  
1 5